



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/928,420  
Source: IFW0  
Date Processed by STIC: 5/28/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT  
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

## Raw Sequence Listing Error Summary

**ERROR DETECTED**
**SUGGESTED CORRECTION**

SERIAL NUMBER: 10/728,420

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1 Wrapped Nucleic Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned...Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was **not saved** in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. **Per Sequence Rules**, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence:  
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
 (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 This sequence is intentionally skipped  

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence.  
 <210> sequence id number  
 <400> sequence id number  
 000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

**RAW SEQUENCE LISTING**  
PATENT APPLICATION: US/10/728,420

DATE: 05/28/2004  
TIME: 13:16:24

Input Set : D:\Sequence Listing.txt  
Output Set: N:\CRF4\05282004\J728420.raw

```

4 <110> APPLICANT: WOULFE, SUSAN L.
5      JAIN, RITA
6      BURR, AIMEE
8 <120> TITLE OF INVENTION: ENGINEERED FAB' FRAGMENT ANTI-TUMOR
9      NECROSIS FACTOR ALPHA IN COMBINATION WITH DISEASE MODIFYING
10     ANTI-RHEUMATIC DRUGS
12 <130> FILE REFERENCE: 122294-1010
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/728,420
16 <141> CURRENT FILING DATE: 2003-12-05
18 <150> PRIOR APPLICATION NUMBER: US 60/431,053
20 <151> PRIOR FILING DATE: 2002-12-05
22 <160> NUMBER OF SEQ ID NOS: 40 (see following pages)
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0

```

## ERRORED SEQUENCES

```

E--> 164 <210> SEQ ID NO: 11
E--> 211 <210> SEQ ID NO: 83 (see following pages)
424 <210> SEQ ID NO: 98
425 <211> LENGTH: 11 12 shown below
426 <212> TYPE: PRT
427 <213> ORGANISM: Artificial Sequence
429 <220> FEATURE:
430 <223> OTHER INFORMATION: human group 1 consensus framework H4
432 <400> SEQUENCE: 98
433 Trp Gly Gln Gly Thr Thr Leu Val Thr Val Ser Ser
E--> 434 1      5          10
E--> 691 <210> SEQ ID NO: 113
E--> 730 <210> SEQ ID NO: 115 (see following pages)

```

Does Not Comply  
Corrected Diskette Needed

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/728,420

DATE: 05/28/2004  
TIME: 13:16:26

Input Set : D:\Sequence Listing.txt  
Output Set: N:\CRF4\05282004\J728420.raw

Skipped Sequences (NEW RULES) :

Sequence(s) missing. If intentional, please use the following format for each skipped sequence.

<210> sequence id number  
<400> sequence id number  
000

Seq#: 9, 10, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34

Seq#: 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58

Seq#: 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82

Seq#: 110, 111, 112, 114

The above sequences are missing. If intentionally skipped, please use the above format exactly.

(see p.3 for a sample of missing sequences)

10/28/420 3

<400> 8

gac att caa atg acc cag agc cca tcc agc ctg agc gca tct gta gga 48  
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

gac cggtgc acc atc act tgt aaa gcc agt cag aac gta ggt act aac 96  
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
20 25 30

gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa gcc ctc atc 144  
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
35 40 45

tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga 192  
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly  
50 55 60

tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca 240  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc 288  
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
85 90 95

aca ttc ggt cag ggt act aaa gta gaa atc aaa 321  
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
100 105

*Sequences 9 and 10 are missing*

<210> 11

See p. 4

10/728,420 4

<210> 1  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> hTNF40 CDRH1

? please give source of genetic material

Please connect any subsequent sequences  
with this type of explanation.

See item 11 on Error Summary Sheet.

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/728,420

DATE: 05/28/2004

TIME: 13:16:26

Input Set : D:\Sequence Listing.txt

Output Set: N:\CRF4\05282004\J728420.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number  
L:134 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:164 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 9 thru 10  
L:177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11  
L:211 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 12 thru 82  
L:434 M:252 E: No. of Seq. differs, <211> LENGTH:Input:11 Found:12 SEQ:98  
L:529 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:533 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:101  
L:552 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:102  
L:576 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:103  
L:600 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:104  
L:624 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:105  
L:691 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 110 thru 112  
L:730 M:214 E: (33) Seq.# missing, SEQ ID NO:114